

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Pulst, Stefan M.
- (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR ATAXIA-2 AND PRODUCTS RELATED THERETO
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
(B) STREET: 444 South Flower Street, Suite 2000
(C) CITY: Los Angeles
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 90071
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Ramos, Robert T.
(B) REGISTRATION NUMBER: 37,915
(C) REFERENCE/DOCKET NUMBER: P07 37217
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 213-622-7700
(B) TELEFAX: 213-489-4210

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | |
|---|-----|
| TTGGTAGCAA CGGAAACGGC GCGGCGCGT TTCGGCCCCG CTCCCGGCGG CTCCTTGGTC | 60 |
| TCGGCGGGCC TCCCCGCCCC TTCGTCGTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC | 120 |
| CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCC TCGTCCCCG CCGCGTTCCG | 180 |
| GCGTCTCCTT GCGCGCCCCG GCTCCCGGCT GTCCCCGCC GCGTGCGAG CCGGTGTATG | 240 |
| GGCCCCCTAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC | 300 |
| AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA | 360 |

AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCCT	420
CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG	480
GGAGGCCCGG CCTGGGCAGG TGGGTGTCGG CACCCC	516

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 163..4101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG	60
GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG	120
CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCGCCCTC CG ATG CGC TCA GCG	174
Met Arg Ser Ala	1
GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC	222
Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe	5 10 15 20
GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG	270
Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg	25 30 35
CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC	318
Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser	40 45 50
GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG AGC	366
Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln Ser	55 60 65
TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC	414
Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly	70 75 80
GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGC CCT	462
Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro	85 90 95 100
CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC	510
Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala	105 110 115
CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC	558
Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser	120 125 130
CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC	606
Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro	135 140 145

CGC Arg	CCG Pro 150	GCG Ala	TGC Cys	GAG Glu	CCG Pro	GTG Val 155	TAT Tyr	GGG Gly	CCC Pro	CTC Leu	ACC Thr 160	ATG Met	TCG Ser	CTG Leu	AAG Lys	654
CCC Pro 165	CAG Gln	CAG Gln	CAG Gln	CAG Gln	CAG Gln 170	CAG Gln	CAG Gln	CAG Gln	CAA Gln	CAG Gln 175	CAG Gln	CAG Gln	CAG Gln	CAA Gln	CAG Gln 180	702
CAG Gln	CAG Gln	CAG Gln	CAG Gln	CAG Gln 185	CAG Gln	CAG Gln	CCG Pro	CCG Pro	CCC Pro 190	GCG Ala	GCT Ala	GCC Ala	AAT Asn	GTC Val 195	CGC Arg	750
AAG Lys	CCC Pro	GGC Gly	GGC Gly 200	AGC Ser	GGC Gly	CTT Leu	CTA Leu	GCG Ala 205	TCG Ser	CCC Pro	GCC Ala	GCC Ala	GCG Ala 210	CCT Pro	TCG Ser	798
CCG Pro	TCC Ser	TCG Ser 215	TCC Ser	TCG Ser	GTC Val	TCC Ser	TCG Ser 220	TCC Ser	TCG Ser	GCC Ala	ACG Thr	GCT Ala 225	CCC Pro	TCC Ser	TCG Ser	846
GTG Val 230	GTC Val	GCG Ala	GCG Ala	ACC Thr	TCC Ser	GGC Gly 235	GGC Gly	GGG Gly	AGG Arg	CCC Pro	GGC Gly 240	CTG Leu	GGC Gly	AGA Arg	GGT Gly	894
CGA Arg 245	AAC Asn	AGT Ser	AAC Asn	AAA Lys	GGA Gly 250	CTG Leu	CCT Pro	CAG Gln	TCT Ser	ACG Thr 255	ATT Ile	TCT Ser	TTT Phe	GAT Asp	GGA Gly 260	942
ATC Ile	TAT Tyr	GCA Ala	AAT Asn	ATG Met 265	AGG Arg	ATG Met	GTT Val	CAT His	ATA Ile 270	CTT Leu	ACA Thr	TCA Ser	GTT Val 275	GTT Val	GGC Gly	990
TCC Ser	AAA Lys	TGT Cys	GAA Glu 280	GTA Val	CAA Gln	GTG Val	AAA Lys 285	AAT Asn	GGA Gly	GGT Gly	ATA Ile	TAT Tyr	GAA Glu 290	GGA Gly	GTT Val	1038
TTT Phe	AAA Lys	ACT Thr 295	TAC Tyr	AGT Ser	CCG Pro	AAG Lys	TGT Cys 300	GAT Asp	TTG Leu	GTA Val	CTT Leu	GAT Asp 305	GCC Ala	GCA Ala	CAT His	1086
GAG Glu 310	AAA Lys	AGT Ser	ACA Thr	GAA Glu	TCC Ser	AGT Ser 315	TCG Ser	GGG Gly	CCG Pro	AAA Lys 320	CGT Arg	GAA Glu	GAA Glu	ATA Ile	ATG Met	1134
GAG Glu 325	AGT Ser	ATT Ile	TTG Leu	TTC Phe	AAA Lys 330	TGT Cys	TCA Ser	GAC Asp	TTT Phe	GTT Val 335	GTG Val	GTA Val	CAG Gln	TTT Phe	AAA Lys 340	1182
GAT Asp	ATG Met	GAC Asp	TCC Ser	AGT Ser 345	TAT Tyr	GCA Ala	AAA Lys	AGA Arg	GAT Asp 350	GCT Ala	TTT Phe	ACT Thr	GAC Asp	TCT Ser 355	GCT Ala	1230
ATC Ile	AGT Ser	GCT Ala	AAA Lys 360	GTG Val	AAT Asn	GGC Gly	GAA Glu	CAC His 365	AAA Lys	GAG Glu	AAG Lys	GAC Asp	CTG Leu 370	GAG Glu	CCC Pro	1278
TGG Trp	GAT Asp	GCA Ala 375	GGT Gly	GAA Glu	CTC Leu	ACA Thr	GCC Ala 380	AAT Asn	GAG Glu	GAA Glu	CTT Leu	GAG Glu 385	GCT Ala	TTG Leu	GAA Glu	1326
AAT Asn 390	GAC Asp	GTA Val	TCT Ser	AAT Asn	GGA Gly	TGG Trp 395	GAT Asp	CCC Pro	AAT Asn	GAT Asp	ATG Met 400	TTT Phe	CGA Arg	TAT Tyr	AAT Asn	1374
GAA Glu 405	GAA Glu	AAT Asn	TAT Tyr	GGT Gly	GTA Val 410	GTG Val	TCT Ser	ACG Thr	TAT Tyr	GAT Asp 415	AGC Ser	AGT Ser	TTA Leu	TCT Ser	TCG Ser 420	1422

TAT	ACA	GTG	CCC	TTA	GAA	AGA	GAT	AAC	TCA	GAA	GAA	TTT	TTA	AAA	CGG	1470
Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	Ser	Glu	Glu	Phe	Leu	Lys	Arg	
				425					430					435		
GAA	GCA	AGG	GCA	AAC	CAG	TTA	GCA	GAA	GAA	ATT	GAG	TCA	AGT	GCC	CAG	1518
Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	Glu	Ile	Glu	Ser	Ser	Ala	Gln	
			440					445					450			
TAC	AAA	GCT	CGA	GTG	GCC	CTG	GAA	AAT	GAT	GAT	AGG	AGT	GAG	GAA	GAA	1566
Tyr	Lys	Ala	Arg	Val	Ala	Leu	Glu	Asn	Asp	Asp	Arg	Arg	Glu	Glu	Glu	
		455					460					465				
AAA	TAC	ACA	GCA	GTT	CAG	AGA	AAT	TCC	AGT	GAA	CGT	GAG	GGG	CAC	AGC	1614
Lys	Tyr	Thr	Ala	Val	Gln	Arg	Asn	Ser	Ser	Glu	Arg	Glu	Gly	His	Ser	
	470					475					480					
ATA	AAC	ACT	AGG	GAA	AAT	AAA	TAT	ATT	CCT	CCT	GGA	CAA	AGA	AAT	AGA	1662
Ile	Asn	Thr	Arg	Glu	Asn	Lys	Tyr	Ile	Pro	Pro	Gly	Gln	Arg	Asn	Arg	
485					490					495					500	
GAA	GTC	ATA	TCC	TGG	GGA	AGT	GGG	AGA	CAG	AAT	TCA	CCG	CGT	ATG	GGC	1710
Glu	Val	Ile	Ser	Trp	Gly	Ser	Gly	Arg	Gln	Asn	Ser	Pro	Arg	Met	Gly	
				505					510					515		
CAG	CCT	GGA	TCG	GGC	TCC	ATG	CCA	TCA	AGA	TCC	ACT	TCT	CAC	ACT	TCA	1758
Gln	Pro	Gly	Ser	Gly	Ser	Met	Pro	Ser	Arg	Ser	Thr	Ser	His	Thr	Ser	
			520					525					530			
GAT	TTC	AAC	CCG	AAT	TCT	GGT	TCA	GAC	CAA	AGA	GTA	GTT	AAT	GGA	GGT	1806
Asp	Phe	Asn	Pro	Asn	Ser	Gly	Ser	Asp	Gln	Arg	Val	GTT	Asn	Gly	Gly	
		535					540					545				
GTT	CCC	TGG	CCA	TCG	CCT	TGC	CCA	TCT	CCT	TCC	TCT	CGC	CCA	CCT	TCT	1854
Val	Pro	Trp	Pro	Ser	Pro	Cys	Pro	Ser	Pro	Ser	Ser	Arg	Pro	Pro	Ser	
	550					555						560				
CGC	TAC	CAG	TCA	GGT	CCC	AAC	TCT	CTT	CCA	CCT	CGG	GCA	GCC	ACC	CCT	1902
Arg	Tyr	Gln	Ser	Gly	Pro	Asn	Ser	Leu	Pro	Pro	Arg	Ala	Ala	Thr	Pro	
565					570					575					580	
ACA	CGG	CCG	CCC	TCC	AGG	CCC	CCC	TCG	CGG	CCA	TCC	AGA	CCC	CCG	TCT	1950
Thr	Arg	Pro	Pro	Ser	Arg	Pro	Pro	Ser	Arg	Pro	Ser	Arg	Pro	Pro	Ser	
				585					590					595		
CAC	CCC	TCT	GCT	CAT	GGT	TCT	CCA	GCT	CCT	GTC	TCT	ACT	ATG	CCT	AAA	1998
His	Pro	Ser	Ala	His	Gly	Ser	Pro	Ala	Pro	Val	Ser	Thr	Met	Pro	Lys	
			600					605					610			
CGC	ATG	TCT	TCA	GAA	GGG	CCT	CCA	AGG	ATG	TCC	CCA	AAG	GCC	CAG	CGA	2046
Arg	Met	Ser	Ser	Glu	Gly	Pro	Pro	Arg	Met	Ser	Pro	Lys	Ala	Gln	Arg	
			615				620					625				
CAT	CCT	CGA	AAT	CAC	AGA	GTT	TCT	GCT	GGG	AGG	GGT	TCC	ATA	TCC	AGT	2094
His	Pro	Arg	Asn	His	Arg	Val	Ser	Ala	Gly	Arg	Gly	Ser	Ile	Ser	Ser	
	630					635					640					
GGC	CTA	GAA	TTT	GTA	TCC	CAC	AAC	CCA	CCC	AGT	GAA	GCA	GCT	ACT	CCT	2142
Gly	Leu	Glu	Phe	Val	Ser	His	Asn	Pro	Pro	Ser	Glu	Ala	Ala	Thr	Pro	
645					650					655					660	
CCA	GTA	GCA	AGG	ACC	AGT	CCC	TCG	GGG	GGA	ACG	TGG	TCA	TCA	GTG	GTC	2190
Pro	Val	Ala	Arg	Thr	Ser	Pro	Ser	Gly	Gly	Thr	Trp	Ser	Ser	Val	Val	
				665					670					675		
AGT	GGG	GTT	CCA	AGA	TTA	TCC	CCT	AAA	ACT	CAT	AGA	CCC	AGG	TCT	CCC	2238
Ser	Gly	Val	Pro	Arg	Leu	Ser	Pro	Lys	Thr	His	Arg	Pro	Arg	Ser	Pro	
			680					685					690			

AGA Arg	CAG Gln	AAC Asn 695	AGT Ser	ATT Ile	GGA Gly	AAT Asn 700	ACC Thr	CCC Pro	AGT Ser	GGG Gly	CCA Pro	GTT Val 705	CTT Leu	GCT Ala	TCT Ser	2286
CCC Pro	CAA Gln 710	GCT Ala	GGT Gly	ATT Ile	ATT Ile	CCA Pro 715	ACT Thr	GAA Glu	GCT Ala	GTT Val	GCC Ala 720	ATG Met	CCT Pro	ATT Ile	CCA Pro	2334
GCT Ala 725	GCA Ala	TCT Ser	CCT Pro	ACG Thr	CCT Pro 730	GCT Ala	AGT Ser	CCT Pro	GCA Ala	TCG Ser 735	AAC Asn	AGA Arg	GCT Ala	GTT Val	ACC Thr 740	2382
CCT Pro	TCT Ser	AGT Ser	GAG Glu	GCT Ala 745	AAA Lys	GAT Asp	TCC Ser	AGG Arg	CTT Leu 750	CAA Gln	GAT Asp	CAG Gln	AGG Arg	CAG Gln	AAC Asn 755	2430
TCT Ser	CCT Pro	GCA Ala	GGG Gly 760	AAT Asn	AAA Lys	GAA Glu	AAT Asn	ATT Ile 765	AAA Lys	CCC Pro	AAT Asn	GAA Glu	ACA Thr 770	TCA Ser	CCT Pro	2478
AGC Ser	TTC Phe	TCA Ser 775	AAA Lys	GCT Ala	GAA Glu	AAC Asn	AAA Lys 780	GGT Gly	ATA Ile	TCA Ser	CCA Pro	GTT Val 785	GTT Val	TCT Ser	GAA Glu	2526
CAT His 790	AGA Arg	AAA Lys	CAG Gln	ATT Ile	GAT Asp	GAT Asp 795	TTA Leu	AAG Lys	AAA Lys	TTT Phe	AAG Lys 800	AAT Asn	GAT Asp	TTT Phe	AGG Arg	2574
TTA Leu 805	CAG Gln	CCA Pro	AGT Ser	TCT Ser	ACT Thr 810	TCT Ser	GAA Glu	TCT Ser	ATG Met	GAT Asp 815	CAA Gln	CTA Leu	CTA Leu	AAC Asn	AAA Lys 820	2622
AAT Asn	AGA Arg	GAG Glu	GGA Gly 825	GAA Lys	AAA Ser	TCA Arg	AGA Arg	GAT Asp	TTG Leu 830	ATC Ile	AAA Lys	GAC Asp	AAA Lys	ATT Ile	GAA Glu 835	2670
CCA Pro	AGT Ser	GCT Ala	AAG Lys 840	GAT Asp	TCT Ser	TTC Phe	ATT Ile	GAA Glu 845	AAT Asn	AGC Ser	AGC Ser	AGC Ser	AAC Asn 850	TGT Cys	ACC Thr	2718
AGT Ser	GGC Gly	AGC Ser 855	AGC Ser	AAG Lys	CCG Pro	AAT Asn	AGC Ser 860	CCC Pro	AGC Ser	ATT Ile	TCC Ser 865	CCT Pro	TCA Ser	ATA Ile	CTT Leu	2766
AGT Ser	AAC Asn 870	ACG Thr	GAG Glu	CAC His	AAG Lys	AGG Arg 875	GGA Gly	CCT Pro	GAG Glu	GTC Val	ACT Thr 880	TCC Ser	CAA Gln	GGG Gly	GTT Val	2814
CAG Gln 885	ACT Thr	TCC Ser	AGC Ser	CCA Pro	GCA Ala 890	TGT Cys	AAA Lys	CAA Gln	GAG Glu	AAA Lys 895	GAC Asp	GAT Asp	AAG Lys	GAA Glu	GAG Glu 900	2862
AAG Lys	AAA Lys	GAC Asp	GCA Ala	GCT Ala 905	GAG Glu	CAA Gln	GTT Val	AGG Arg	AAA Lys 910	TCA Ser	ACA Thr	TTG Leu	AAT Asn	CCC Pro 915	AAT Asn	2910
GCA Ala	AAG Lys	GAG Glu	TTC Phe 920	AAC Asn	CCA Pro	CGT Arg	TCC Ser	TTC Phe	TCT Ser	CAG Gln	CCA Pro	AAG Lys	CCT Pro 930	TCT Ser	ACT Thr	2958
ACC Thr	CCA Pro	ACT Thr 935	TCA Ser	CCT Pro	CGG Arg	CCT Pro	CAA Gln 940	GCA Ala	CAA Gln	CCT Pro	AGC Ser	CCA Pro 945	TCT Ser	ATG Met	GTG Val	3006
GGT Gly	CAT His 950	CAA Gln	CAG Gln	CCA Pro	ACT Thr	CCA Pro 955	GTT Val	TAT Tyr	ACT Thr	CAG Gln	CCT Pro 960	GTT Val	TGT Cys	TTT Phe	GCA Ala	3054

CCA Pro 965	AAT Asn	ATG Met	ATG Met	TAT Tyr	CCA Pro 970	GTC Val	CCA Pro	GTG Val	AGC Ser	CCA Pro 975	GGC Gly	GTG Val	CAA Gln	CCT Pro	TTA Leu 980	3102
TAC Tyr	CCA Pro	ATA Ile	CCT Pro	ATG Met 985	ACG Thr	CCC Pro	ATG Met	CCA Pro	GTG Val 990	AAT Asn	CAA Gln	GCC Ala	AAG Lys	ACA Thr 995	TAT Tyr	3150
AGA Arg	GCA Ala	GTA Val	CCA Pro 1000	AAT Asn	ATG Met	CCC Pro	CAA Gln	CAG Arg 1005	CGG Arg	CAA Gln	GAC Asp	CAG Gln	CAT His 1010	CAT His	CAG Gln	3198
AGT Ser	GCC Ala	ATG Met 1015	ATG Met	CAC His	CCA Pro	GCG Ala	TCA Ser 1020	GCA Ala	GCG Ala	GGC Gly	CCA Pro 1025	CCG Pro	ATT Ile	GCA Ala	GCC Ala	3246
ACC Thr	CCA Pro 1030	CCA Pro	GCT Ala	TAC Tyr	TCC Ser	ACG Thr 1035	CAA Gln	TAT Tyr	GTT Val	GCC Ala 1040	TAC Tyr	AGT Ser	CCT Pro	CAG Gln	CAG Gln	3294
TTC Phe 1045	CCA Pro	AAT Asn	CAG Gln	CCC Pro	CTT Leu 1050	GTT Val	CAG Gln	CAT His	GTG Val	CCA Pro 1055	CAT His	TAT Tyr	CAG Gln	TCT Ser	CAG Gln 1060	3342
CAT His	CCT Pro	CAT His	GTC Val	TAT Tyr 1065	AGT Ser	CCT Pro	GTA Val	ATA Ile	CAG Gln 1070	GGT Gly	AAT Asn	GCT Ala	AGA Arg	ATG Met 1075	ATG Met	3390
GCA Ala	CCA Pro	CCA Pro	ACA Thr 1080	CAC His	GCC Ala	CAG Gln	CCT Pro	GGT Gly 1085	TTA Leu	GTA Val	TCT Ser	TCT Ser	TCA Ser 1090	GCA Ala	ACT Thr	3438
CAG Gln	TAC Tyr	GGG Gly 1095	GCT Ala	CAT His	GAG Glu	CAG Gln	ACG Thr 1100	CAT His	GCG Ala	ATG Met	TAT Tyr 1105	GCA Ala	TGT Cys	CCC Pro	AAA Lys	3486
TTA Leu 1110	CCA Pro	TAC Tyr	AAC Asn	AAG Lys	GAG Glu 1115	ACA Thr	AGC Ser 1115	CCT Pro	TCT Ser	TTC Phe 1120	TAC Tyr	TTT Phe	GCC Ala	ATT Ile	TCC Ser	3534
ACG Thr 1125	GGC Gly	TCC Ser	CTT Leu	GCT Ala	CAG Gln 1130	CAG Gln	TAT Tyr	GCG Ala	CAC His	CCT Pro 1135	AAC Asn	GCT Ala	ACC Thr	CTG Leu	CAC His 1140	3582
CCA Pro	CAT His	ACT Thr	CCA Pro	CAC His 1145	CCT Pro	CAG Gln	CCT Pro	TCA Ser	GCT Ala 1150	ACC Thr	CCC Pro	ACT Thr	GGA Gly	CAG Gln 1155	CAG Gln	3630
CAA Gln	AGC Ser	CAA Gln	CAT His 1160	GGT Gly	GGA Gly	AGT Ser	CAT His	CCT Pro 1165	GCA Ala	CCC Pro	AGT Ser	CCT Pro	GTT Val 1170	CAG Gln	CAC His	3678
CAT His	CAG Gln	CAC His	CAG Gln	GCC Ala	GCC Ala	CAG Gln	GCT Ala 1180	CTC Leu	CAT His	CTG Leu	GCC Ala	AGT Ser 1185	CCA Pro	CAG Gln	CAG Gln	3726
CAG Gln 1190	TCA Ser	GCC Ala	ATT Ile	TAC Tyr	CAC His	GCG Ala 1195	GGG Gly	CTT Leu	GCG Ala	CCA Pro	ACT Thr 1200	CCA Pro	CCC Pro	TCC Ser	ATG Met	3774
ACA Thr 1205	CCT Pro	GCC Ala	TCC Ser	AAC Asn	ACG Thr 1210	CAG Gln	TCG Ser	CCA Pro	CAG Gln	AAT Asn 1215	AGT Ser	TTC Phe	CCA Pro	GCA Ala 1220	GCA Ala	3822
CAA Gln	CAG Gln	ACT Thr	GTC Val	TTT Phe 1225	ACG Thr	ATC Ile	CAT His	CCT Pro	TCT Ser 1230	CAC His	GTT Val	CAG Gln	CCG Pro	GCG Ala	TAT Tyr 1235	3870

ACC AAC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA CAG TCA	3918
Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala His Val Gln Ser	
1240 1245 1250	
GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG CTA ATG	3966
Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met Leu Met	
1255 1260 1265	
ACG ACA CAG CCA CCC GGC GGT CCC CAG GCC GCC CTC GCT CAA AGT GCA	4014
Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu Ala Gln Ser Ala	
1270 1275 1280	
CTA CAG CCC ATT CCA GTC TCG ACA ACA GCG CAT TTC CCC TAT ATG ACG	4062
Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr Met Thr	
1285 1290 1295 1300	
CAC CCT TCA GTA CAA GCC CAC CAC CAA CAG CAG TTG TAAGGCTGCC	4108
His Pro Ser Val Gln Ala His His Gln Gln Leu	
1305 1310	
CTGGAGGAAC CGAAAGGCCA AATTCCTCC TCCCTTCTAC TGCTTCTACC AACTGGAAGC	4168
ACAGAAACT AGAATTTTCAT TTATTTTGTT TTTAAATAT ATATGTTGAT TTCTTGTAAC	4228
ATCCAATAGG AATGCTAACA GTTCACTTGC AGTGGAAGAT ACTTGACCG AGTAGAGGCA	4288
TTTAGGAACT TGGGGGCTAT TCCATAATTC CATATGCTGT TTCAGAGTCC CGCAGGTACC	4348
CCAGCTCTGC TTGCCGAAAC TGGAAGTTAT TTATTTTTTA ATAACCCTTG AAAGTCATGA	4408
ACACATCAGC TAGCAAAAGA AGTAACAAGA GTGATTCTTG CTGCTATTAC TGCTAAAAAA	4468
AAAAAAAAA AAA	4481

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Arg Ser Ala Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu	
1 5 10 15	
Ser Arg Arg Phe Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln	
20 25 30	
Arg Pro Ala Arg Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly	
35 40 45	
Pro Tyr Pro Ser Ala Ala Pro Pro Pro Gly Pro Gly Pro Pro Pro	
50 55 60	
Ser Arg Gln Ser Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn	
65 70 75 80	
Gly Asn Gly Gly Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly	
85 90 95	
Leu Gly Gly Pro Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala	
100 105 110	

Ser	Pro	Gly	Ala	Pro	Pro	Ala	Ala	Pro	Thr	Arg	Ala	Ser	Pro	Leu	Gly
		115					120					125			
Ala	Arg	Ala	Ser	Pro	Pro	Arg	Ser	Gly	Val	Ser	Leu	Ala	Arg	Pro	Ala
		130					135					140			
Pro	Gly	Cys	Pro	Arg	Pro	Ala	Cys	Glu	Pro	Val	Tyr	Gly	Pro	Leu	Thr
		145				150					155				160
Met	Ser	Leu	Lys	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln
				165						170				175	
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Ala	Ala
			180					185					190		
Ala	Asn	Val	Arg	Lys	Pro	Gly	Gly	Ser	Gly	Leu	Leu	Ala	Ser	Pro	Ala
		195					200					205			
Ala	Ala	Pro	Ser	Pro	Ser	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ser	Ala	Thr
		210				215					220				
Ala	Pro	Ser	Ser	Val	Val	Ala	Ala	Thr	Ser	Gly	Gly	Gly	Arg	Pro	Gly
		225			230					235					240
Leu	Gly	Arg	Gly	Arg	Asn	Ser	Asn	Lys	Gly	Leu	Pro	Gln	Ser	Thr	Ile
				245					250					255	
Ser	Phe	Asp	Gly	Ile	Tyr	Ala	Asn	Met	Arg	Met	Val	His	Ile	Leu	Thr
			260					265					270		
Ser	Val	Val	Gly	Ser	Lys	Cys	Glu	Val	Gln	Val	Lys	Asn	Gly	Gly	Ile
		275					280					285			
Tyr	Glu	Gly	Val	Phe	Lys	Thr	Tyr	Ser	Pro	Lys	Cys	Asp	Leu	Val	Leu
		290				295					300				
Asp	Ala	Ala	His	Glu	Lys	Ser	Thr	Glu	Ser	Ser	Ser	Gly	Pro	Lys	Arg
		305			310					315					320
Glu	Glu	Ile	Met	Glu	Ser	Ile	Leu	Phe	Lys	Cys	Ser	Asp	Phe	Val	Val
				325					330					335	
Val	Gln	Phe	Lys	Asp	Met	Asp	Ser	Ser	Tyr	Ala	Lys	Arg	Asp	Ala	Phe
			340					345					350		
Thr	Asp	Ser	Ala	Ile	Ser	Ala	Lys	Val	Asn	Gly	Glu	His	Lys	Glu	Lys
		355					360					365			
Asp	Leu	Glu	Pro	Trp	Asp	Ala	Gly	Glu	Leu	Thr	Ala	Asn	Glu	Glu	Leu
		370				375					380				
Glu	Ala	Leu	Glu	Asn	Asp	Val	Ser	Asn	Gly	Trp	Asp	Pro	Asn	Asp	Met
		385			390					395					400
Phe	Arg	Tyr	Asn	Glu	Glu	Asn	Tyr	Gly	Val	Val	Ser	Thr	Tyr	Asp	Ser
			405						410					415	
Ser	Leu	Ser	Ser	Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	Ser	Glu	Glu
			420					425					430		
Phe	Leu	Lys	Arg	Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	Glu	Ile	Glu
		435					440					445			
Ser	Ser	Ala	Gln	Tyr	Lys	Ala	Arg	Val	Ala	Leu	Glu	Asn	Asp	Asp	Arg
		450				455					460				

Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg
 465 470 475 480
 Glu Gly His Ser Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly
 485 490 495
 Gln Arg Asn Arg Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser
 500 505 510
 Pro Arg Met Gly Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr
 515 520 525
 Ser His Thr Ser Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val
 530 535 540
 Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser
 545 550 555 560
 Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg
 565 570 575
 Ala Ala Thr Pro Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser
 580 585 590
 Arg Pro Pro Ser His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser
 595 600 605
 Thr Met Pro Lys Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro
 610 615 620
 Lys Ala Gln Arg His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly
 625 630 635 640
 Ser Ile Ser Ser Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu
 645 650 655
 Ala Ala Thr Pro Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp
 660 665 670
 Ser Ser Val Val Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg
 675 680 685
 Pro Arg Ser Pro Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro
 690 695 700
 Val Leu Ala Ser Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala
 705 710 715 720
 Met Pro Ile Pro Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn
 725 730 735
 Arg Ala Val Thr Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp
 740 745 750
 Gln Arg Gln Asn Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn
 755 760 765
 Glu Thr Ser Pro Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro
 770 775 780
 Val Val Ser Glu His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys
 785 790 795 800
 Asn Asp Phe Arg Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln
 805 810 815

Leu Leu Asn Lys Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys
 820 825 830
 Asp Lys Ile Glu Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser
 835 840 845
 Ser Asn Cys Thr Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser
 850 855 860
 Pro Ser Ile Leu Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr
 865 870 875 880
 Ser Gln Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp
 885 890 895
 Asp Lys Glu Glu Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr
 900 905 910
 Leu Asn Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro
 915 920 925
 Lys Pro Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser
 930 935 940
 Pro Ser Met Val Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro
 945 950 955 960
 Val Cys Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly
 965 970 975
 Val Gln Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln
 980 985 990
 Ala Lys Thr Tyr Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp
 995 1000 1005
 Gln His His Gln Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro
 1010 1015 1020
 Pro Ile Ala Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr
 1025 1030 1035 1040
 Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His
 1045 1050 1055
 Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn
 1060 1065 1070
 Ala Arg Met Met Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser
 1075 1080 1085
 Ser Ser Ala Thr Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr
 1090 1095 1100
 Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr
 1105 1110 1115 1120
 Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn
 1125 1130 1135
 Ala Thr Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro
 1140 1145 1150
 Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser
 1155 1160 1165

Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala
 1170 1175 1180

Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr
 1185 1190 1195 1200

Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser
 1205 1210 1215

Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val
 1220 1225 1230

Gln Pro Ala Tyr Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala
 1235 1240 1245

His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro
 1250 1255 1260

Met Met Leu Met Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu
 1265 1270 1275 1280

Ala Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe
 1285 1290 1295

Pro Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
 1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

G CAC GAG GGG CCG CTC ACC ATG TCG CTG AAG CCG CAG CCG CAG CCG	46
His Glu Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Pro Gln Pro	
1 5 10 15	
CCC GCG CCC GCC ACT GGC CGC AAG CCC GGC GGC GGC CTG CTC TCG TCG	94
Pro Ala Pro Ala Thr Gly Arg Lys Pro Gly Gly Gly Leu Leu Ser Ser	
20 25 30	
CCC GGC GCC GCG CCG GCC TCG GCC GCG GTG ACC TCG GCT TCC GTG GTG	142
Pro Gly Ala Ala Pro Ala Ser Ala Ala Val Thr Ser Ala Ser Val Val	
35 40 45	
CCG GCC CCG GCC GCG CCG GTG GCG TCT TCC TCG GCG GCC GCG GGC GGC	190
Pro Ala Pro Ala Ala Pro Val Ala Ser Ser Ser Ala Ala Ala Gly Gly	
50 55 60	
GGG CGT CCC GGC CTG GGC AGA GGT CGG AAC AGT AGC AAA GGA CTG CCT	238

Gly	Arg 65	Pro	Gly	Leu	Gly	Arg 70	Gly	Arg	Asn	Ser	Ser 75	Lys	Gly	Leu	Pro	
CAG Gln 80	CCT Pro	ACG Thr	ATT Ile	TCT Ser	TTT Phe 85	GAT Asp	GGA Gly	ATC Ile	TAT Tyr	GCA Ala 90	AAC Asn	GTG Val	AGG Arg	ATG Met	GTT Val 95	286
CAT His	ATA Ile	CTT Leu	ACG Thr	TCA Ser 100	GTT Val	GTT Val	GGA Gly	TCG Ser	AAA Lys 105	TGT Cys	GAA Glu	GTA Val	CAA Gln	GTG Val 110	AAA Lys	334
AAC Asn	GGA Gly	GGC Gly	ATA Ile 115	TAT Tyr	GAA Glu	GGA Gly	GTT Val	TTT Phe 120	AAA Lys	ACA Thr	TAC Tyr	AGT Ser	CCT Pro 125	AAG Lys	TGT Cys	382
GAC Asp	TTG Leu	GTA Val 130	CTT Leu	GAT Asp	GCT Ala	GCA Ala	CAT His 135	GAG Glu	AAA Lys	AGT Ser	ACA Thr	GAA Glu 140	TCC Ser	AGT Ser	TCG Ser	430
GGG Gly	CCA Pro 145	AAA Lys	CGT Arg	GAA Glu	GAA Glu	ATA Ile 150	ATG Met	GAG Glu	AGT Ser	GTT Val	TTG Leu 155	TTC Phe	AAA Lys	TGC Cys	TCA Ser	478
GAC Asp 160	TTC Phe	GTT Val	GTG Val	GTA Val	CAG Gln 165	TTT Phe	AAA Lys	GAT Asp	ACA Thr	GAC Asp 170	TCC Ser	AGT Ser	TAT Tyr	GCA Ala	CGG Arg 175	526
AGA Arg	GAT Asp	GCT Ala	TTT Phe	ACT Thr 180	GAC Asp	TCT Ser	GCT Ala	CTC Leu	AGC Ser 185	GCA Ala	AAG Lys	GTG Val	AAT Asn	GGT Gly 190	GAG Glu	574
CAC His	AAG Lys	GAG Glu	AAG Lys 195	GAC Asp	CTG Leu	GAG Glu	CCC Pro	TGG Trp 200	GAT Asp	GCA Ala	GGG Gly	GAG Glu	CTC Leu 205	ACG Thr	GCC Ala	622
AGC Ser	GAG Glu	GAG Glu	CTG Leu	GAG Glu	CTG Leu	GAG Glu	AAT Asn 215	GAT Asp	GTG Val	TCT Ser	AAT Asn	GGA Gly 220	TGG Trp	GAC Asp	CCC Pro	670
AAT Asn 225	GAC Asp	ATG Met	TTT Phe	CGA Arg	TAT Tyr	AAT Asn 230	GAA Glu	GAG Glu	AAT Asn	TAT Tyr	GGT Gly 235	GTG Val	GTG Val	TCC Ser	ACA Thr	718
TAT Tyr 240	GAT Asp	AGC Ser	AGT Ser	TTA Leu	TCT Ser 245	TCA Ser	TAT Tyr	ACG Thr	GTT Val	CCT Pro 250	TTA Leu	GAA Glu	AGG Arg	GAC Asp	AAC Asn 255	766
TCA Ser	GAA Glu	GAA Glu	TTT Phe	CTT Leu 260	AAA Lys	CGG Arg	GAG Glu	GCA Ala	AGG Arg 265	GCA Ala	AAC Asn	CAG Gln	TTA Leu	GCA Ala 270	GAA Glu	814
GAA Glu	ATT Ile	GAA Glu	TCC Ser 275	AGT Ser	GCT Ala	CAG Gln	TAC Tyr	AAA Lys 280	GCT Ala	CGT Arg	GTC Val	GCC Ala	CTT Leu 285	GAG Glu	AAT Asn	862
GAT Asp	GAC Asp	CGG Arg 290	AGT Ser	GAG Glu	GAA Glu	GAA Glu	AAA Lys 295	TAC Tyr	ACA Thr	GCA Ala	GTC Val	CAG Gln 300	AGA Arg	AAC Asn	TGC Cys	910
AGT Ser	GAC Asp 305	CGG Arg	GAG Glu	GGG Gly	CAT His	GGC Gly 310	CCC Pro	AAC Asn	ACT Thr	AGG Arg	GAC Asp 315	AAT Asn	AAA Lys	TAT Tyr	ATT Ile	958
CCT Pro 320	CCT Pro	GGA Gly	CAA Gln	AGA Arg	AAC Asn 325	AGA Arg	GAA Glu	GTC Val	CTA Leu	TCC Ser 330	TGG Trp	GGA Gly	AGT Ser	GGG Gly	AGA Arg 335	1006

CAG	AGC	TCA	CCA	CGG	ATG	GGC	CAG	CCT	GGG	CCA	GGC	TCC	ATG	CCG	TCA	1054
Gln	Ser	Ser	Pro	Arg	Met	Gly	Gln	Pro	Gly	Pro	Gly	Ser	Met	Pro	Ser	
				340					345					350		
AGA	GCT	GCT	TCT	CAC	ACT	TCA	GAT	TTC	AAC	CCG	AAC	GCT	GGC	TCA	GAC	1102
Arg	Ala	Ala	Ser	His	Thr	Ser	Asp	Phe	Asn	Pro	Asn	Ala	Gly	Ser	Asp	
			355					360					365			
CAA	AGA	GTA	GTT	AAT	GGA	GGT	GTT	CCC	TGG	CCA	TCG	CCT	TGC	CCA	TCT	1150
Gln	Arg	Val	Val	Asn	Gly	Gly	Val	Pro	Trp	Pro	Ser	Pro	Cys	Pro	Ser	
		370					375					380				
CCT	TCC	TCT	CGC	CCA	CCT	TCT	CGC	TAC	CAG	TCA	GGT	CCC	AAC	TCT	CTT	1198
Pro	Ser	Ser	Arg	Pro	Pro	Ser	Arg	Tyr	Gln	Ser	Gly	Pro	Asn	Ser	Leu	
	385					390					395					
CCA	CCT	CGG	GCA	GCC	ACC	CCT	ACA	CGG	CCT	CGT	GCC	GAA	TTC	CTG	CAG	1246
Pro	Pro	Arg	Ala	Ala		Pro	Thr	Arg	Pro	Arg	Ala	Glu	Phe	Leu	Gln	
400					405					410					415	
CCC	GGG	GAT	CC													1257
Pro	Gly	Asp														

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

His	Glu	Gly	Pro	Leu	Thr	Met	Ser	Leu	Lys	Pro	Gln	Pro	Gln	Pro	Pro	
1				5					10					15		
Ala	Pro	Ala	Thr	Gly	Arg	Lys	Pro	Gly	Gly	Gly	Leu	Leu	Ser	Ser	Pro	
			20					25					30			
Gly	Ala	Ala	Pro	Ala	Ser	Ala	Ala	Val	Thr	Ser	Ala	Ser	Val	Val	Pro	
		35				40						45				
Ala	Pro	Ala	Ala	Pro	Val	Ala	Ser	Ser	Ser	Ala	Ala	Ala	Gly	Gly	Gly	
	50					55					60					
Arg	Pro	Gly	Leu	Gly	Arg	Gly	Arg	Asn	Ser	Ser	Lys	Gly	Leu	Pro	Gln	
65				70				75						80		
Pro	Thr	Ile	Ser	Phe	Asp	Gly	Ile	Tyr	Ala	Asn	Val	Arg	Met	Val	His	
				85				90					95			
Ile	Leu	Thr	Ser	Val	Val	Gly	Ser	Lys	Cys	Glu	Val	Gln	Val	Lys	Asn	
			100					105					110			
Gly	Gly	Ile	Tyr	Glu	Gly	Val	Phe	Lys	Thr	Tyr	Ser	Pro	Lys	Cys	Asp	
		115					120					125				
Leu	Val	Leu	Asp	Ala	Ala	His	Glu	Lys	Ser	Thr	Glu	Ser	Ser	Ser	Gly	
	130					135					140					
Pro	Lys	Arg	Glu	Glu	Ile	Met	Glu	Ser	Val	Leu	Phe	Lys	Cys	Ser	Asp	
145					150					155					160	

[illegible]